

(1) GENERAL INFORMATION

(i) APPLICANT: LIN, LEU-FEN  
COLLINS, FRANKLIN D.  
DOHERTY, DANIEL H.  
LILE, JACK  
BEKTESH, SUSAN

(ii) TITLE OF INVENTION: Glial Cell Line-Derived  
Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: AMGEN INC.  
(B) STREET: One Amgen Center Drive  
(C) CITY: Thousand Oaks  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy Disk  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: 7.1  
(D) SOFTWARE: Microsoft Word for WIN 7.0a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/182,183  
(B) FILING DATE: 23-MAY-1994

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: N-terminal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa  
5 10 15

Gln Ala Ala Ala Ala Ser Pro Asp Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal fragment

(ix) FEATURE: Xaa is either Lys or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu  
5 10

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: nucleic acid for rat GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCCCGGGCT GCAGGAATTC GGGG GTC TAC GGA GAC CGG ATC CGA GGT      48
                               Val Tyr Gly Asp Arg Ile Arg Gly
                               -90

GCC GCC GCC GGA CGG GAC TCT AAG ATG AAG TTA TGG GAT GTC GTG      93
Ala Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val
-85 -80 -75

GCT GTC TGC CTG GTG TTG CTG CAC ACC GCG TCT GCC TTC CCG CTG      138
Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu
-70 -65 -60

CCC GCC GGT AAG AGG CTT CTC GAA GCG CCC GCC GAA GAC CAC TCC      183
Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser
-55 -50 -45

CTC GGC CAC CGC CGC GTG CCC TTC GCG CTG ACC AGT GAC TCC AAT      228
Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn
-40 -35 -30

ATG CCC GAA GAT TAT CCT GAC CAG TTT GAT GAC GTC ATG GAT TTT      273
Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe
-25 -20 -15

ATT CAA GCC ACC ATC AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA      318
Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln
-10 -5 1 5

GCG GCG GCA CTT CCT CGA AGA GAG AGG AAC CGG CAA GCT GCA GCT      363
Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala
10 15 20

GCC AGC CCA GAG AAT TCC AGA GGG AAA GGT CGC AGA GGC CAG AGG      408
Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
25 30 35
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GGC AAA AAT CGG GGG TGC GTC TTA ACT GCA ATA CAC TTA AAT GTC	453
Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val	
40 45 50	
ACT GAC TTG GGT TTG GGC TAC GAA ACC AAG GAG GAA CTG ATC TTT	498
Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe	
55 60 65	
CGA TAT TGT AGC GGT TCC TGT GAA GCG GCC GAG ACA ATG TAC GAC	543
Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp	
70 75 80	
AAA ATA CTA AAA AAT CTG TCT CGA AGT AGA AGG CTA ACA AGT GAC	588
Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp	
85 90 95	
AAG GTA GGC CAG GCA TGT TGC AGG CCG GTC GCC TTC GAC GAC GAC	633
Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp	
100 105 110	
CTG TCG TTT TTA GAC GAC AGC CTG GTT TAC CAT ATC CTA AGA AAG	678
Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys	
115 120 125	
CAT TCC GCT AAA CGG TGT GGA TGT ATC TGA CCCTGGCTCC	718
His Ser Ala Lys Arg Cys Gly Cys Ile	
130	
AGAGACTGCT GTGTATTGCA TTCCTGCTAC ACTGCGAAGA AAGGGACCAA	768
GGTTCCCAGG AAATATTTGC CCAGAAAGGA AGATAAGGAC CAAGAAGGCA	818
GAGGCAGAGG CGGAAGAAGA AGAAGAAAAG AAGGACGAAG GCAGCCATCT	868
GTGGGAGCCT GTAGAAGGAG GCCCAGCTAC AG	900

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: inferred amino acid sequence for mature rat GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
1 5 10 15
Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
20 25 30

Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	
		35					40					45				
Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	
	50					55					60					
Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	
65					70					75					80	
Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	
				85					90					95		
Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	
			100					105					110			
Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	
		115					120					125				
Lys	Arg	Cys	Gly	Cys	Ile											

- (2) INFORMATION FOR SEQ ID NO:5
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ix) FEATURE:
- (A) NAME/KEY: nucleic acid sequence for human GDNF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTT TCTCTTTTCT TTTTGAACAG CA AAT ATG CCA GAG GAT TAT CCT	47
Ser Asn Met Pro Glu Asp Tyr Pro	
-25 -20	
GAT CAG TTC GAT GAT GTC ATG GAT TTT ATT CAA GCC ACC ATT	89
Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile	
-15 -10	
AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA ATG GCA GTG CTT	131
Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu	
-5 1 5	
CCT AGA AGA GAG CGG AAT CGG CAG GCT GCA GCT GCC AAC CCA	173
Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro	
10 15 20	
GAG AAT TCC AGA GGA AAA GGT CGG AGA GGC CAG AGG GGC AAA	215
Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys	
25 30 35	

AAC CGG GGT TGT GTC TTA ACT GCA ATA CAT TTA AAT GTC ACT	257
Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr	
40 45 50	
GAC TTG GGT CTG GGC TAT GAA ACC AAG GAG GAA CTG ATT TTT	299
Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe	
55 60 65	
AGG TAC TGC AGC GGC TCT TGC GAT GCA GCT GAG ACA ACG TAC	341
Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr	
70 75	
GAC AAA ATA TTG AAA AAC TTA TCC AGA AAT AGA AGG CTG GTG	383
Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val	
80 85 90	
ACT GAC AAA GTA GGG CAG GCA TGT TGC AGA CCC ATC GCC TTT	425
Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe	
95 100 105	
GAT GAT GAC CTG TCG TTT TTA GAT GAT AAC CTG GTT TAC CAT	467
Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His	
110 115 120	
ATT CTA AGA AAG CAT TCC GCT AAA AGG TGT GGA TGT ATC TGA	509
Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile	
125 130	
CTCCGGCTCC AGAGACTGCT GTGTATTGCA TTCCTGCTAC AGTGCAAAGA	559
AAG	562

(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: inferred amino acid sequence for mature human GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
1 5 10 15
Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
20 25 30
Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
35 40 45

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile  
50 55 60

Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp  
65 70 75 80

Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys  
85 90 95

Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser  
100 105 110

Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala  
115 120 125

Lys Arg Cys Gly Cys Ile  
130

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide probe
- (D) OTHER INFORMATION: N at positions 3, 15, and 18 is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCNGAYAARC ARGCNGCNGC

20

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: nucleic acid sequence for human GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCTCTCCCC CACCTCCCGC CTGCCCCGCGC A GGT GCC GCC GCC GGA 46  
Gly Ala Ala Ala Gly  
-5

CGG GAC TTT AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC 88  
Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys  
1 5 10

CTG GTG CTG CTC CAC ACC GCG TCC GCC TTC CCG CTG CCC GCC 130  
Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala  
15 20

GGT AAG AGG CCT CCC GAG GCG CCC GCC GAA GAC CGC TCC CTC 172  
 Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu  
 25 30 35

GGC CGC CGC CGC GCG CCC TTC GCG CTG AGC AGT GAC T 209  
 Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp  
 40 45 50

GTAAGAACCG TTCC 223

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGAATTCG GG 12

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Asp Lys Gln Ala Ala Ala  
 5

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: nucleic acid sequence from pBluescript SK-76.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGGAACC GGCAAGCTGC WGMWGYMWGM CCW 33

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Arg Asn Arg Gln Ala Ala Ala Ser Pro  
5 10

(2) INFORMATION FOR SEQ ID NO:13

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide DHD-26
- (D) OTHER INFORMATION: N at positions 9 and 12 are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ARRTTYTTNA RNATYTTRTC

20

(2) INFORMATION FOR SEQ ID NO:14

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acid residues
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asp Lys Ile Leu Lys Asn Leu  
5

(2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: oligonucleotide primer PD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GACGGGACTC TAAGATG

17

(2) INFORMATION FOR SEQ ID NO:16

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: oligonucleotide primer DHD23

(D) OTHER INFORMATION: N at positions 3, 6, and 18 is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCNGCNGCYT GYTTRTCNGG

20

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide primer LF2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGAGACAATG TACGACA

17

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide primer PD2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCTGGAGCC AGGGTCA

17

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide primer PD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCCGAATTCG ACGGGACTCT AAGATG

26

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer LFA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGTGGCCAG AGGGAGTGGT CTTC

24

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGATCCA ATAAGGAGGA AAAAAAATGT CACCAGATAA ACAAAT

46

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCGGTACCC AGTCTCTGGA GCCGGA

26

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: adapter fragment for plasmid pCJ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCTAGAAT TGTCATGTTT GACAGCTTAT CAT

33

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: polylinker sequence for plasmid pCJX1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

AATTCCCGGG TACCAGATCT GAGCTCACTA GTCTGCA

37

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: nucleic acid sequence for human GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

TTCTCTCCCC CACCTCCCGC CTGCCCCGCGC A GGT GCC GCC GCC GGA	46
Gly Ala Ala Ala Gly	
CGG GAC TTT AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC	88
Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys	
CTG GTG CTG CTC CAC ACC GCG TCC GCC TTC CCG CTG CCC GCC	130
Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala	
GGT AAG AGG CCT CCC GAG GCG CCC GCC GAA GAC CGC TCC CTC	172
Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu	
GGC CGC CGC CGC GCG CCC TTC GCG CTG AGC AGT GAC TCA AAT	214
Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn	
ATG CCA GAG GAT TAT CCT GAT CAG TTC GAT GAT GTC ATG GAT	256
Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp	
TTT ATT CAA GCC ACC ATT AAA AGA CTG AAA AGG TCA CCA GAT	298
Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp	
1	
AAA CAA ATG GCA GTG CTT CCT AGA AGA GAG CGG AAT CGG CAG	340
Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln	
5 10 15	
GCT GCA GCT GCC AAC CCA GAG AAT TCC AGA GGA AAA GGT CGG	382
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg	
20 25 30	
AGA GGC CAG AGG GGC AAA AAC CGG GGT TGT GTC TTA ACT GCA	424
Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala	
35 40 45	
ATA CAT TTA AAT GTC ACT GAC TTG GGT CTG GGC TAT GAA ACC	466
Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr	
50 55	

AAG	GAG	GAA	CTG	ATT	TTT	AGG	TAC	TGC	AGC	GGC	TCT	TGC	GAT	508
Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	
60					65					70				

GCA	GCT	GAG	ACA	ACG	TAC	GAC	AAA	ATA	TTG	AAA	AAC	TTA	TCC	550
Ala	Ala	Glu	Thr	Thr	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	
75					80					85				

AGA	AAT	AGA	AGG	CTG	GTG	ACT	GAC	AAA	GTA	GGG	CAG	GCA	TGT	592
Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	
	90					95						100		

TGC	AGA	CCC	ATC	GCC	TTT	GAT	GAT	GAC	CTG	TCG	TTT	TTA	GAT	634
Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	
		105						110					115	

GAT	AAC	CTG	GTT	TAC	CAT	ATT	CTA	AGA	AAG	CAT	TCC	GCT	AAA	676
Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	
			120						125					

AGG	TGT	GGA	TGT	ATC	TGA	CTCCGGCTCC	AGAGACTGCT	GTGTATTGCA	724
Arg	Cys	Gly	Cys	Ile					
130									

TTCCTGCTAC	AGTGCAAAGA	AAG	747
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(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Ala Ala Ala Gly  
5

Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys  
10 15

Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala  
20 25 30

Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu  
35 40 45

Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn  
50 55 60

Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp  
65 70 75

Phe	Ile	Gln	Ala	Thr	Ile	Lys	Arg	Leu	Lys	Arg	Ser	Pro	Asp	80	85	
Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg	Gln	90	95	100
Ala	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	105	110	115
Arg	Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	120	125	130
Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	135	140	145
Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	150	155	
Ala	Ala	Glu	Thr	Thr	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	160	165	170
Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	175	180	185
Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	190	195	200
Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	205	210	215
Arg	Cys	Gly	Cys	Ile										220		